



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/936,883
Source: PCT/09
Date Processed by STIC: 10/4/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/936,883

DATE: 10/04/2001
TIME: 10:11:25

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\10042001\I936883.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Miyata, Toshio
6 <120> TITLE OF INVENTION: A METHOD FOR DETECTING MEGSIN PROTEIN
7 AND USE THEREOF
9 <130> FILE REFERENCE: SHIM012
OK 11 <140> CURRENT APPLICATION NUMBER: US/09/936,883
OK 12 <141> CURRENT FILING DATE: 2001-09-07
14 <150> PRIOR APPLICATION NUMBER: PCT/JP00/01646
15 <151> PRIOR FILING DATE: 2000-03-17
17 <150> PRIOR APPLICATION NUMBER: 11/75305
18 <151> PRIOR FILING DATE: 1999-03-19
20 <150> PRIOR APPLICATION NUMBER: 11/306623
21 <151> PRIOR FILING DATE: 1999-10-28
23 <160> NUMBER OF SEQ ID NOS: 21
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1867
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <400> SEQUENCE: 1
33 atggcctccc ttgctqcagc aaatqcagq ttttgcctca acctgttcmt aasruaaaaaa 60
E--> 34 aasnnaaguhc yshashuhag agagatggat gacaatcaag gaaatggaaa tgtgttctt 120 → see item 9 on Error summary sheet
E--> 35 tcctctargg umtasasash gngyasngya snvahhsrsr ctgagccctct tcgctgcctt 180
E--> 36 ggccctggtc cgcttggcg ctcagatus ruhaaaaaaa uvaarguguya agnasgactc 240
E--> 37 cctctctcag attgataagt tgcttcatgt taacactgcc tcaassrusr gnasysuuhs 300
E--> 38 vaasnthaas srggatatgg aaactcttct aatagtcagt cagggtctcca gtctcaactg 360
E--> 39 gytyrgyasn srsrasnsrg nsrgyugnsr gnuaaaaagag tttttctga tataaatgca 420
E--> 40 tcccacacaagg attatgatct cysargvhah rasasnaasr hsysastyra suagcatttg 480
E--> 41 gaatgggctt tttgctgaaa aagtgtatgg ctgcataag srvaasngyu haaguyvat 540
E--> 42 yrgyhhsysg actacattga gtgtgccgaa aaattatacy atgccaaagt ggagcgaast 600
E--> 43 yrgucysaag uysutyrasa aysvaguaro qttgacttta cqaatcattt agaagacact 660
E--> 44 agacgtataa ttaataagva ashthrasnh suguasthra rgargasnas nystgggttg 720
E--> 45 aaaatgaaac acatggcaaa atcaagaacg tgattggta atrvaguasn guthrhsgyy 780
E--> 46 sysasnvagy guggtggcat aagctcatct gctgtatgg tgctggtaa tgctgtgtac 840
E--> 47 gygysrsrsr aavamtvauv aasnaavaty rttcaaaggc aagtggcaat cagccttcac 900
E--> 48 caagagcgaa accataaaath ysgyystrgn sraahthrys srguthrasn tgccatttca 960
E--> 49 aatctccaa gtgctctggg aaggcagtcg ccatgatgcy shshyssrry scyssrgyys 1020
E--> 50 aavaaaamtmt catcagaac ggaqatcaa tttqtctgtt attgaggacc catcaatghs 1080
E--> 51 gnuguargysh asnusrvagu asrsrmtaag attcttgagc tcagatcacaa tgggtggcata 1140
E--> 52 aacatgtacg ttctgysugu uargtvrasn gygyasnmmt yrvauctgcc tgagaatgac 1200
E--> 53 ctctctgaaa ttgaaaacaa actgacccctt cagurguasn asusrgugua snysuthrhg 1260
E--> 54 naatctaattg gaatggacca atccaaaggcg aatgacccctt aagtatgtta snumtguutr 1320
E--> 55 hrasnrarga rgmtthrsry styrvagagg tatttttcc tcagttcaag atagagaaga 1380
E--> 56 attatgaaat gaaaguvahh rgnhysguys asntyrgumt yscaatattt gagagcccta 1440

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E--> 57 ~~gggctgaaag atatcttga tgaatccaaa qntyruarga augyuysash asgusrysgc~~ 1500 item 9
 58 agatctctct gggattgcct cggggggctcg tctgtatata tcaaggaas usrgyaasrg 1560
 59 ygyargutyr srargatgt gcacaaatct tacatagagg tcactgagga gggcaccgag 1620
 60 qctmtmthsy ssrtyruva thrgugugyt hrquaactg ctgccacagg aagtaatatt 1680
 E--> 61 ~~gtagaaaagc aactccctca gtccthraaa athrgysras nvaguysgnu rgnsracgct~~ 1740 item 9
 62 gtttagagct gaccaccat tcctatgt tatcaggaag gatthruhar gaaashsrhu 1800
 63 hvaargysas gacatcatct tattcagtgg caaagttct tgcccttggaa suhsrgyysv 1860
 64 asrcysr 1867

all 9 item 9
 313 <210> SEQ ID NO: 18
 314 <211> LENGTH: 1938
 315 <212> TYPE: RNA
 316 <213> ORGANISM: Rattus norvegicus
 318 <400> SEQUENCE: 18

E--> 319 ~~tttcaaaaatg gcctcccttg ctgcagcaaa tgcaaaaa ttggcttcgacm taasruaaaa~~ 60
 E--> 320 ~~aaashaaagh gyhasttatt cagagagatg gatagtagtc aaggaaacgg aaatgtatcc~~ 120
 E--> 321 ~~ttcuuharggu mtassrsrgn gyasnngasn vahhtcttcc ctgagcatct tcactgcct~~ 180
 E--> 322 ~~gagcctaatac cgtttgggtg ctsrsrusrh thraausrua rgugyaacga ggtgactgt~~ 240
 E--> 323 ~~nncgtcagat tgacaaggcc ctgcacttta tctccarggy ascysaaarg gnasysaauh~~ 300
 E--> 324 ~~shsrccatca agacaaggga attcatcgaa cagtcagcta ggactgcaat atrsrarggn~~ 360
 E--> 325 ~~gyasnrsrsa snsrgnugyu gntyrcattt gaaaagagtt cttgctgaca taaactcatc~~ 420
 E--> 326 ~~tcataaggat nnngnuysar gvauaaasas nsrsrhysa saaaaactca gcattgcca~~ 480
 E--> 327 ~~tggagtttt gcagagaaaag tatttgcattt tysusraas ngyvahaagu ysvahashca~~ 540
 E--> 328 ~~taagagctat atggagtgtg ctgaaaactt atacaatgtc aaagtghsys srtymrtguc~~ 600
 E--> 329 ~~ysaaguasnu tyrasnaays vagaaagagt tgattttaca aatgatatac aagaaaccag~~ 660
 E--> 330 ~~atttaaaatt guargvaash thrasnasn guthrarghy saataaatgg attgaaaatg~~ 720
 E--> 331 ~~aacacacatgg caaaatcaag aaggtgttga snystruas nguthrhsgy yssysvaug~~ 780
 E--> 332 ~~gggacagcag cctcagctca tcagctgtca tggctgtatc gaatgctgya ssrsrusrs~~ 840
 E--> 333 ~~sraavamtva uvaasnnaagt ttacttcaaa ggcaagtggaa aatcggcctt caccaagagt~~ 900
 E--> 334 ~~gataccvaty rhysgyystr yssraahthr yssrasthrc tcagttgcca tttcaggct~~ 960
 E--> 335 ~~cccagcggtc ctggaaaagc agttaatusr cyshshargs rrsrgyrgyy saavaasn~~ 1020
 E--> 336 ~~gatgcataa gaacggaggt tcaatttgc taccatttc gagccamtmt hsgnguarga~~ 1080
 E--> 337 ~~rghasnusrt hrngurcca atgcagattc ttgagctaca atatcatggt ggcataagca~~ 1140
 E--> 338 ~~tgtacrmtn uguugntyhr sgygysrmtt yratcatgtt gcccggaggat gacctatcc~~ 1200
 E--> 339 ~~aaattgaaag caagctgagt mturguasas usrgugusry susrttccag aatctaattgg~~ 1260
 E--> 340 ~~actggacaaa tagcaggaag atgaaatctc aghgnasnum tastrthras nsrargysmt~~ 1320
 E--> 341 ~~yssrgntatg tgaatgtgtt tctccccag ttcaagatag agaaagatta tgaatyrvaa~~ 1380
 E--> 342 ~~snvhurghn ysguysasty rguatgagga gccacttggaa atctgttaggc ttgaaagaca~~ 1440
 E--> 343 ~~tcttttgttgc gmtargsrhs uyssrvagyu guashvagut ccagggtctga tctgtctgg~~ 1500
 E--> 344 ~~attgcctctg gaggtcgtct ctatgtasra rgaaasusrg yaasrgygya rgutyrvatc~~ 1560
 E--> 345 ~~aaagctaattg cacaagtccc tcataagatgt ctcagaagaa ggcaccsrys umthsyssru~~ 1620
 E--> 346 ~~guvasrgugu gythrgaggc aactgctgcc acagaaagta acatcggtga aaagctactt~~ 1680
 E--> 347 ~~cctguathr aaaathrgus rasnvaguys uurgaatcca cggtgttccag agctgaccgc~~ 1740
 E--> 348 ~~ccctttctgt ttgtcattag ggusrthrv ahargaasar grhuhvaarg aagaatggca~~ 1800
 E--> 349 ~~tcatcttatt tactggaaa gtctcggtc ctysasngu hthrgyysva srcysrtgaa~~ 1860
 E--> 350 ~~attcttattt gttttccata cactaacagg catgaagaaa catcataagt gaatagaatt~~ 1920
 E--> 351 ~~gtatattggaa gtacatgg~~ 1938

353 <210> SEQ ID NO: 19
 354 <211> LENGTH: 380
 355 <212> TYPE: PRT

"T's not allowed in an RNA sequence
Per 1.823 of Sequence Rules, a Combined DNA/RNA sequence requires a C 2127 response of DNA; also, explain in C2207-C2237 section that sequence is a combined DNA/RNA

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Input Set : A:\seqlist.txt

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356 <213> ORGANISM: Rattus norvegicus
 358 <400> SEQUENCE: 19
 359 Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Gly Phe Asp Leu Phe
 360 1 5 10 15
 361 Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe Ser Ser
 362 20 25 30
 363 Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala Arg Gly
 364 35 40 45
 E--> 365 Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser
 366 50 55 60
 367 Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu
 368 65 70 75 80
 E--> 369 Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu
 370 85 90 95
 371 Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys
 372 100 105 110
 373 Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg
 374 115 120 125
 375 Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys
 376 130 135 140
 377 Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp
 378 145 150 155 160
 379 Ser Ser Leu Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
 380 165 170 175
 381 Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser
 382 180 185 190
 383 Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met
 384 195 200 205
 385 His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met
 386 210 215 220
 387 Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr Ile Met
 388 225 230 235 240
 389 Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln
 390 245 250 255
 391 Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val
 392 260 265 270
 393 Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg
 394 275 280 285
 395 Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg
 396 290 295 300
 397 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys
 398 305 310 315 320
 399 Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala
 400 325 330 335
 401 Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser
 402 340 345 350
 403 Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg Lys Asn
 404 355 360 365
 405 Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

All item 9
 on Error
 summary
 sheet

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Input Set : A:\seqlist.txt
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406	370	375	380	
409 <210> SEQ ID NO: 20				
410 <211> LENGTH: 1848				
411 <212> TYPE: DNA				
412 <213> ORGANISM: Mus Musculus				
414 <400> SEQUENCE: 20				
415 ttcgacttat tcagagagat ggatagtagc caaggaaatg gaaatgtaha suharggumt 60				→ all
E--> 416 assrsrgngy asnygashva ttcttcttt ccctgagcat cttcaactgcc ctgaccctaa 120				item 9
417 tccgtctghh srsrusrhth raauthruar qugqtgctcg aggtgactgt gcacgtcaga 180				
E--> 418 ttgacaaggc actgcacttt gyaaarggya scysaaargg nasysauhs haacatacca 240				item 9
E--> 419 tcaaagacaag gaaactcatac taataatcag ccaggactta snrsrarggn gyasnsrsra 300				
E--> 420 snasngnrgy ucagtatcaa ttgaaaagag ttcttgctga cataaaactca tctcataagg 360				
E--> 421 ntyrgnuysa rgvauuaasa snsrsrhsys gattatgaac tcagcattgc cactggagtt 420				item 9
422 ttgcagaaaa aagtctatas tyrguusraa thrgyvahaa guysvatyrg actttcataa 480				
E--> 423 gaactacatt gagtgctgctg aaaacttata caatgctash hsysasntyr gucysaagua 540				
E--> 424 snutyrasna aaaagtggaa agagttgact tcacaaatga tgtacaagat accagattt 600				
E--> 425 svaguargva ashthrasna svagnasthr arghaaaatt aataaatgga ttgaaaatga 660				
E--> 426 gacacatgga aagatcaaga agysasnyst rguasnguth rhsgyssy sgtqttggg 720				
427 gacagcagcc tcagctcgtc ggctgtcatg gtgcgttgtv augyassrsr usrsrsraav 780				
E--> 428 amtvauvaaa cgctgtttac ttcaaaggca aatgaaatc ggccttcacc aagactasna 840				
429 avatyrhyss yystryssra ahthrysthr gataccctca gttgccgtt taggtctccc 900				
430 acgtgtcctg gaaaagtaas thrusrcysa rghargsrrt hrcysrgyys vagttaatat 960				
E--> 431 gatgcataaa gaaeggeggt tcaattttgc taceatttcag vaasnmtmth snguargar 1020				item 9
E--> 432 ghasnusrh rgnacccac caatgcaggt tcttgagctc caatatcatg gtggcataag 1080				
E--> 433 cgnrrrmtnv auguugntyr hsgygysrat gtacattatg ctgcctgagg atggctata 1140				
434 taaaatttga aagcaagmtt rmturguasg yucysgugus rysctgagtt tccagaatct 1200				
E--> 435 gatggactgg accaatagga gaaaaatgaa ausrhgnasn umtastrthr ashargargy 1260				item 9
E--> 436 smtystctca gtatgtgaac gtgtttctcc cccagttcaa gatagagaag aatsrgntyr 1320				
E--> 437 vaasnvhur gnhysguysa stntatgaaat gacgaccac ttgaaaatct taggcttqaa 1380				
438 agatatctt tyrgumtthr hshsuysru gyuysashga tgagtccagt gcagatctct 1440				
439 ctggatttgc ctctggaggt cgtctcasgu srsraaasus rgyaasrgy yargutacgt 1500				
440 atcaaagcta atgcacaagt cattcataga ggtctcagag gagtyrvavr ysumthsyss 1560				
441 rhquvasrgu guggcaactga agccactgct qccacagaaa ataacattgt tgaaaagcag 1620				item 9
E--> 442 gythrguaat hraaaathrg uasnasnvg uysgnettee tgagtccaca gtgttcagag 1680				
443 ccgaccgccc ctctgttt gtcuqrusrt hrhargaa asargruhv aatcaagaag 1740				
E--> 444 aatgacateea tcttattttac tggcaaagtc tcttgctcty sysasnasuh thrgyssvas 1800				item 9
445 rcysrtgaaa ttcgatttgg ttcctatac agtaacaggc atcaagaa 1848				

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

PMJ

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/936,883

DATE: 10/04/2001
TIME: 10:11:26

Input Set : A:\seqlist.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:132 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:132 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:137 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:144 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:144 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:156 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:156 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:161 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:218 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:319 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:15
L:320 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:320 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:320 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:27
M:340 Repeated in SeqNo=18
L:321 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:321 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:39
L:322 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:322 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:50
L:323 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:323 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:59
L:324 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:324 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:68
L:325 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:325 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:79
L:326 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:326 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:85
L:327 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
L:327 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:99
L:328 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15
L:328 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:114
L:329 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:329 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:124
L:330 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:330 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:136
L:331 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
L:331 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:143
L:332 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:332 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:154
L:333 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:333 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:165
L:334 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13

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Input Set : A:\seqlist.txt
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L:334 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:178
L:335 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:335 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:184
L:336 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13
L:336 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:197
L:337 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:337 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:209
L:338 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13
L:338 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:222
L:339 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:339 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:232
L:340 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:340 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:241
L:341 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16
L:341 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:257
L:342 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:342 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:266
L:343 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13
L:343 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:279
L:344 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:344 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:291
L:345 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:345 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:299
L:346 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:346 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:309
L:347 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:347 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:317
L:348 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:348 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:329
L:349 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15
L:349 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:344
L:350 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:19
L:350 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:363
L:351 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:351 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:368
L:365 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
M:340 Repeated in SeqNo=19
L:416 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
M:340 Repeated in SeqNo=20

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/936,883</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	